



#4

SEQUENCE LISTING

<110> BROWN, Eric L.
LEE, Lawrence
HOOK, Magnus

<120> METHOD OF PREVENTING T CELL-MEDIATED RESPONSES BY THE USE OF THE MAJOR HISTOCOMPATIBILITY COMPLEX CLASS II ANALOG PROTEIN (MAP PROTEIN) FROM STAPHYLOCOCCUS AUREUS

<130> P07023US01/BAS

<140> 10/041,775

<141> 2002-01-10

<150> 60/260,523

<151> 2001-01-10

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 603

<212> DNA

<213> Staphylococcus aureus

<220>

<221> CDS

<222> (1)...(603)

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Thr Ile Thr Val Asn Gly Thr Ser Gln Asn Ile Leu Ser Ser Leu Thr
20 25 30

96

ttt aat aag aat caa caa att agt tat aaa gat ata gag aat aaa gtt
Phe Asn Lys Asn Gln Gln Ile Ser Tyr Lys Asp Ile Glu Asn Lys Val
35 40 45

144

aaa tca gtt tta tac ttt aat aga ggt att agt gat atc gat tta aga
Lys Ser Val Leu Tyr Phe Asn Arg Gly Ile Ser Asp Ile Asp Leu Arg
50 55 60

192

ctt tct aag caa gca aaa tac acg gtt cat ttt aag aat gga aca aaa
Leu Ser Lys Gln Ala Lys Tyr Thr Val His Phe Lys Asn Gly Thr Lys
65 70 75 80

240

aga gtt gtc gat ttg aaa gca ggc att cac aca gcc gac tta atc aat
Arg Val Val Asp Leu Lys Ala Gly Ile His Thr Ala Asp Leu Ile Asn
85 90 95

288

aca agt gac att aaa gca att agt gtt aac gta gat act aaa aag caa	336
Thr Ser Asp Ile Lys Ala Ile Ser Val Asn Val Asp Thr Lys Lys Gln	
100 105 110	
gtg aaa gat aaa gag gca aaa gca aat gtt caa gtg ccg tat aca atc	384
Val Lys Asp Lys Glu Ala Lys Ala Asn Val Gln Val Pro Tyr Thr Ile	
115 120 125	
act gtg aat ggt aca agc caa aac att tta tca aac tta aca ttt aaa	432
Thr Val Asn Gly Thr Ser Gln Asn Ile Leu Ser Asn Leu Thr Phe Lys	
130 135 140	
aag aat cag caa att agt tat aaa gat tta gag aat aat gta aaa tca	480
Lys Asn Gln Gln Ile Ser Tyr Lys Asp Leu Glu Asn Asn Val Lys Ser	
145 150 155 160	
gtt tta aaa tca aac aga ggt ata act gat gta gat tta aga ctt tca	528
Val Leu Lys Ser Asn Arg Gly Ile Thr Asp Val Asp Leu Arg Leu Ser	
165 170 175	
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Lys Gln Ala Lys Phe Thr Val Asn Phe Lys Asn Gly Thr Lys Lys Val	
180 185 190	
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Ile Asp Leu Lys Ala Gly Ile Tyr	
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Phe Asn Lys Asn Gln Gln Ile Ser Tyr Lys Asp Ile Glu Asn Lys Val	
35 40 45	

Lys Ser Val Leu Tyr Phe Asn Arg Gly Ile Ser Asp Ile Asp Leu Arg	
50 55 60	

Leu Ser Lys Gln Ala Lys Tyr Thr Val His Phe Lys Asn Gly Thr Lys	
65 70 75 80	

Arg Val Val Asp Leu Lys Ala Gly Ile His Thr Ala Asp Leu Ile Asn
85 90 95

Thr Ser Asp Ile Lys Ala Ile Ser Val Asn Val Asp Thr Lys Lys Gln
100 105 110

Val Lys Asp Lys Glu Ala Lys Ala Asn Val Gln Val Pro Tyr Thr Ile
115 120 125

Thr Val Asn Gly Thr Ser Gln Asn Ile Leu Ser Asn Leu Thr Phe Lys
130 135 140

Lys Asn Gln Gln Ile Ser Tyr Lys Asp Leu Glu Asn Asn Val Lys Ser
145 150 155 160

Val Leu Lys Ser Asn Arg Gly Ile Thr Asp Val Asp Leu Arg Leu Ser
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Lys Gln Ala Lys Phe Thr Val Asn Phe Lys Asn Gly Thr Lys Lys Val
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Ile Asp Leu Lys Ala Gly Ile Tyr
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Thr Ile Thr Val Asn Gly Thr Ser Gln Asn Ile Leu Ser Ser Leu Thr
20 25 30

ttt aat aag aat caa caa att agt tat aaa gat ata gag aat aaa gtt 144
Phe Asn Lys Asn Gln Gln Ile Ser Tyr Lys Asp Ile Glu Asn Lys Val
35 40 45

aaa tca gtt tta tac ttt aat aga ggt att agt gat atc gat tta aga 192

Lys Ser Val Leu Tyr Phe Asn Arg Gly Ile Ser Asp Ile Asp Leu Arg			
50	55	60	
ctt tct aag caa gca aaa tac acg gtt cat ttt aag aat gga aca aaa			240
Leu Ser Lys Gln Ala Lys Tyr Thr Val His Phe Lys Asn Gly Thr Lys			
65	70	75	80
aga gtt gtc gat ttg aaa gca ggc att cac aca gcc gac tta atc aat			288
Arg Val Val Asp Leu Lys Ala Gly Ile His Thr Ala Asp Leu Ile Asn			
85	90	95	
aca agt gac att aaa gca att agt gtt aac gta gat act aaa aag caa			336
Thr Ser Asp Ile Lys Ala Ile Ser Val Asn Val Asp Thr Lys Lys Gln			
100	105	110	
gtg aaa gat aaa gag gca aaa gca aat gtt gtc gac ctg cag cca agc			384
Val Lys Asp Lys Glu Ala Lys Ala Asn Val Val Asp Leu Gln Pro Ser			
115	120	125	
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Leu Ile Ser			
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Thr Ile Thr Val Asn Gly Thr Ser Gln Asn Ile Leu Ser Ser Leu Thr			
20	25	30	
Phe Asn Lys Asn Gln Gln Ile Ser Tyr Lys Asp Ile Glu Asn Lys Val			
35	40	45	
Lys Ser Val Leu Tyr Phe Asn Arg Gly Ile Ser Asp Ile Asp Leu Arg			
50	55	60	
Leu Ser Lys Gln Ala Lys Tyr Thr Val His Phe Lys Asn Gly Thr Lys			
65	70	75	80
Arg Val Val Asp Leu Lys Ala Gly Ile His Thr Ala Asp Leu Ile Asn			
85	90	95	
Thr Ser Asp Ile Lys Ala Ile Ser Val Asn Val Asp Thr Lys Lys Gln			
100	105	110	

Val Lys Asp Lys Glu Ala Lys Ala Asn Val Val Asp Leu Gln Pro Ser
115 120 125

Leu Ile Ser
130